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NATIONAL ANIMAL
GENETIC RESOURCES

National Animal Germplasm Program

National Animal Genome Research Program

Report of
Committee jointly appointed by
ARS, CSRS

ARS - Administrator - Dr. R. Dean Plowman

CSRS - Administrator - Dr. J. Patrick Jordan

August 20, 1991

U.S.D.A., NAL
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CATALOGING PREP

Implementation Plans for Joint

Animal Germplasm and
Animal Genome Research Program

NATIONAL GENETICS
RESOURCES PROGRAM

Authorized by the
1990 Farm Bill

ARS, CSRS
Committee Report

Prepublication Copy (Draft)
August 20, 1991

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NATIONAL ANIMAL GERMPLASM PROGRAM

NATIONAL ANIMAL GENOME
RESEARCH PROGRAM

SUMMARY

Animal genome research must become a top priority if U.S. animal agriculture is to remain competitive in world markets. Animal genome mapping will directly benefit from the national effort to map the human genome. The rapidly developing tools and techniques for genomic analysis will greatly enhance the current rudimentary genome maps of livestock species. Construction of livestock maps is coupled to immediate practical applications for the improvement of animal health and productivity, and the development of new agricultural products, and thus offers a rapid return on investments in animal biotechnology.

The objective of this USDA-sponsored National Animal Genome Research Program (NAGRP) is to ensure increased agricultural efficiency and profitability by building a foundation of genetic knowledge for the manipulation of genomes to produce animals with desired phenotypes. It is recommended that for each major livestock species, genetic maps of polymorphic loci be developed with sufficient resolution to permit the location, definition and utilization of genes affecting economically important traits. Essential related objectives include the analysis of the fine structure of candidate genes and gene families, the definition of the genetic basis of quantitative trait loci to be used to implement marker-assisted selection, the development of new experimental technologies for utilization of genome information, and finally the expansion of training opportunities. The efficient use of carefully designed biological resources and the development of a broadly based data management system are essential for this effort.

Prioritization of species for genome analysis should be based on economic importance and the anticipated yield of fundamental genetic information about the genome organization and function. A national organizational structure is required to implement this genome program. This will include a USDA Genome Program Leader, a National Animal Genome Program Committee, Species Genome Coordinating Centers, and Species Genome Committees. A major portion of the funding for this effort should be distributed as competitive grants through the USDA/CSRS/NRI and Special Grants; other funds will come from ARS and SAES sources and from commodity/industry groups. Coordination of efficient use of shared experimental resources, and the integration of data collection and dissemination, should be facilitated by the identification and funding of Species Genome Coordinating Centers which may best be accomplished via a Special Grants program. Additional federal budget needs for implementing this program during the first 3 years will be: year 1, \$5.2 million; year 2, \$7.9 million; and year 3, \$10.8 million.

Because of the complexity of this emerging area of science, the NAGRP will require a concentrated and coordinated effort by CSRS, ARS, and the SAES. This effort is likely to require a commitment of the USDA for at least 10 years, although annual reviews of scientific scope and budget are recommended. This research investment will be of paramount importance to the development of healthier, more productive and efficient animals, and of improved animal products for the 21st century.

INTRODUCTION

The NAGRP is crucial to improving the efficiency and profitability of U.S. animal agriculture and to continuing its leadership role in the global food supply. The genomes of cattle, swine, poultry, sheep and certain aquaculture species are replete with diversity, which can be manipulated for increased production in a variety of environments. Moreover, the molecular and genetic tools for understanding these genomes and their manipulation are either in place or developing rapidly. This program will provide increased allocations for research and will support the establishment and distribution of animal resources to optimally develop genome maps. Finally, a relational database will enable ready access to the most current scientific knowledge, and comparative structures, of animal genomes.

Animal genome research is a world-wide enterprise. Several countries have already implemented animal genome projects and are developing resources for the construction of gene maps in certain species. It is imperative that the U.S. program include strong linkages with the international animal genome community.

STRUCTURE AND ORGANIZATION OF THE PROGRAM

The NAGRP and the NAGP will be jointly coordinated and closely linked to national research efforts within ARS and CSRS organized under the NGRP. Linkages will be developed at various program levels, including budget development. The primary leadership will be within CSRS through a designated Genome Program Leader (GPL). The National Animal Genome Program Committee and Species Genome Committees will serve major advisory roles in policy and operational decision making. Species Genome Coordinating Centers will be created with the responsibility to develop a complete genome map for their species; however, the major emphasis of the NAGRP will be on genome mapping research conducted by individual investigators.

- A. CSRS Genome Program Leader (GPL) reports to CSRS Administrator and to ARS Director of National Genetic Resources Program. The GPL directs the NAGRP by organizing and coordinating the National Animal Genome Program Committee, the Species Genome Committee meetings, and the Species Genome Coordinating Centers. He/she provides liaison with NRI Competitive Grants Program, oversees the comparative animal genome database, and is an advocate for animal genome research activities within USDA. The GPL serves as a USDA representative for international animal genome activities, and as a liaison with other genome programs including the NAGP through linkages to the ARS program leader and serving as an ex-officio member of NAGP Program Committee.
- B. National Animal Genome Program Committee will be composed of active scientists with expertise in animal genome research. After initial appointments, the membership will be comprised of the chair of each Species Genome Committee and the Lead Scientist of each Species Coordinating Center with the GPL of NAGRP and the ARS NAGP Program Leader as ex-officio members. This committee will advise the GPL and other USDA administrators regarding research needs and priorities, broad operational policies, standardization of animal gene nomenclature, and guidelines for species databases and for a comparative animal genome database. This committee will facilitate the dissemination of current gene maps and procedures for retrieval of online database information.

C. Species Genome Committees will include members with active genome research programs in specific species. A Chair and executive committee of 3-5 members, including the Coordinating Center Lead Scientist, will be selected from the general membership; the GPL will be an ex-officio member. The Committee will identify reference herds, establish criteria for their acceptance, preservation and use, set priorities for the use of scarce research resources, and identify probe development needs. It will oversee the development of, and data input for, the species database, will authorize access to unpublished data, and will update the species gene map in concert with the Lead Scientist. Other activities include identifying research opportunities within the species, linking national mapping efforts to international mapping activities, and recommending priorities for QTL research within their species.

D. Species Genome Coordinating Centers will be designated by the Administrators of ARS and CSRS following the completion of a competitive scientific review of 5-year research proposals. Centers will be established for each priority species and will be located at SAES, and/or ARS locations, or consist of a consortium of laboratories at such locations. Centers will be established in phases based on species priorities as follows: cattle, swine, chickens, and aquacultural species. Because of their biological relatedness, the Center for cattle might be expanded to include sheep/goat genome data and the Center for chickens, the turkey data.

Important criteria for selecting institutions as Centers include 1) strong genetics programs emphasizing genomic research, 2) a Lead Scientist with broad experience and with an internationally recognized program in gene mapping committed to serve as Director, and 3) an institutional commitment to support continuing Center activities. The Lead Scientist will provide linkage from the Center to the Genome Program Leader and to Species Genome Committees. Other criteria include the following: personnel experienced in gene mapping and familiar with reference herds, facilities for storing and distributing DNA probes and reference materials, development capabilities for DNA probes and gene markers, and computer database development and maintainence. The Centers will serve as a focal point for the activities of scientists conducting mapping research on a given species and will coordinate the development of the species gene map by maintaining a repository of genetic material (DNA and cells) from reference herds, identifying sufficient numbers of publically available probes for completing a 10-20 cM gene map in the species, distributing genetic material and probes to authorized users, and implementing the relational database for its designated species.

E. Individual investigator initiated research will be funded primarily through CSRS competitive awards, ARS and SAES intramural funds, and commodity/industry monies, and will provide the largest and most crucial sector of the genome research program. The resolution of the species genome maps will be enhanced by studies emphasizing physical and comparative genetic mapping through somatic cell genetics, in situ hybridization, and contig cloning. Investigator initiated awards are expected to analyze the fine structure, organization, and control of important candidate genes and gene families, and to dissect and map complex quantitative trait loci. Fundamental scientific studies should

include developing improved techniques for identification of DNA level polymorphisms of large populations, and implementing new biological and statistical approaches for linkage analyses. Such research will contribute directly to overall national and international genome mapping efforts and to targeted studies of marker-assisted selection. As saturation genome maps are obtained in the major agricultural animal species, research interests are expected to diversify and expand beyond mapping to the structure, organization, and control of economically important genes/loci.

F. Fellowships for postdoctoral and sabbatical research will be established to increase the pool of scientists trained in genomic research. The major emphasis will be directed toward training in molecular techniques utilized in gene identification and mapping research and toward new computers programs to facilitate QTL mapping and to implement marker assisted selection.

DATABASES

Databases will be used to compare mapping data within and among species, to define the species genome map, to map phenotypic traits, and to preserve original mapping data for trait analysis and for construction of alternate chromosome maps. Access will be in the public domain with some restrictions for unpublished portions. Databases for each species will be linked and coordinated with international databases. Programs that combine the mapping database with allelic information on phenotypic/germplasm/QTL data must also be developed to map important alleles regulating those traits.

Establishment of individual species databases will be dependent on the current data available for the species, the international mapping effort in that species, funds availability, and priority for overall genome mapping efforts. If international efforts for database production are underway for some species, the new U.S. effort will be coordinated with them, as may be likely for the European PigMAP effort. In the beginning, a simple PC based spreadsheet approach may be best for most species. For priority species a broader based database will be needed. Such an effort will likely require the development of a relational database using object oriented language so that the widest usage of the data will result and so that the current human and mouse genome databases in Sybase can be easily used. It will be designed for easy access by individuals through other computers and for output both as a high quality graphical interface on Internet connections and as character based data. Information for each new species mapping effort will be stored in the format designated by the National Genome Program Committee.

The species database structure will be set up in an object oriented design and will include these data compartments: 1) Raw bits: actual original mapping data, locus assignments, and probe developments; 2) Probes/clones: listing of DNA markers that work in the species; 3) Reference; 4) Nomenclature/ Thesaurus; 5) Species Consensus Map: Current detailed map of each chromosome as agreed upon by species/chromosome committee; and 6) Comparative Species Genome Maps: Relative mapping data for given species presented as maps of other species in comparison to the given species.

Each species database will be developed at the Species Coordinating Center with final responsibility resting with the Species Genome Committee and will be made available to the comparative genome database. Quality control of data input into species database and assignment of new gene map locations must be approved by the Species Genome Committees. Procedures for, and frequency of, information output will be decided by the Species Committees and the National Animal Genome Program Committee. This can include printed updates, computer disk releases of all/some data, and online access.

Development of a comparative genome database will be a high priority, since the human GDB and murine mapping efforts are well advanced. The fastest approach will be to update the comparative mapping program, currently available at the Jackson Lab, for all the livestock species. NAL database personnel will be involved in this effort to ensure accessibility of the database to the public. Later, as NAL enhances its capabilities for genome database handling, it would be given full responsibility for management of all the genomic databases. One all-inclusive database would be set up at NAL in 2-5 years, depending on funding commitments.

IMPLEMENTATION AND FUNDING

Research funding for NAGRP will come from multiple sources with major emphasis on competitive individual investigator awards. Base funding is currently available for limited parts of this program, but the implementation of a coordinated animal genome program will require additional grant funding as well as some targeted funding, such as Special Grants, for the activities of the CSRS Genome Program Leader, National Animal Genome Program Committee, Species Genome Committee, Species Genome Coordinating Centers, and comparative genome database. Since a complete genome map is essential for this program, funding for Centers will be emphasized at the beginning of the program. The program will be implemented according to the following schedule:

- Year 1 - Designate Genome Program Leader (GM-15)
 - Establish National Animal Genome Program Committee and Species Genome Committees for cattle/sheep, swine, chicken/turkeys, and aquacultural species
 - Select and designate Species Genome Coordinating Center for cattle
 - Initiate development of comparative mapping database and of cattle/sheep and swine (in collaboration with PiGMap) databases
 - create Animal Genome Database Office at NAL
 - NRI funded investigator research awards
- Year 2 - Designate Species Genome Coordinating Center for swine
 - NRI funded investigator research awards
- Year 3 - Designate Species Genome Coordinating Center for chickens/turkeys
 - Expand Cattle Genome Coordinating Center to include sheep
 - Develop chicken/turkey database
 - NRI funded investigator research awards
- Year 4 - Designate Species Genome Coordinating Center for aquacultural species
 - Develop aquacultural species database
 - Implement NAL management of all animal databases
 - NRI funded investigator research awards

Years 5 - 10

- Expansion of NRI funded investigator research awards
- Renewal of Species Genome Coordinating Center awards

Draft
 TOTAL USDA NAGRP BUDGET: PRELIMINARY PROJECTIONS
 Years:

	Base Funds	1	2	3	4	5	6	7	8	9	10
(Thousands of dollars, in FY91 \$)											
<u>CSRS Administration</u>											
GPL Salary/Staff	0	200	200	200	200	200	200	200	200	200	200
Travel/Program Costs	0	50	50	50	50	50	50	50	50	50	50
Committees	0	40	40	40	40	40	40	40	40	40	40
Comparative Database	0	250	250	250	250	250	250	250	250	250	250
NAL Database Office	0	150	150	200	300	300	300	300	300	300	300
Coordinating Centers (#)	(0)	(1)	(2)	(3)	(4)	(4)	(4)	(4)	(4)	(4)	(4)
Salaries (#/Center)											
Lead Scientist (1/2)	0	60	120	180	240	240	240	240	240	240	240
Technicians (3)	0	100	200	300	400	400	400	400	400	400	400
Computer Expert (1)	0	80	160	240	320	320	320	320	320	320	320
Computer Facilities	0	50	100	150	200	200	200	200	200	200	200
Reference Herds	0	40	80	120	160	160	160	160	160	160	160
Probe Development	0	100	250	400	550	600	600	600	550	500	450
Storage and Distribution	0	50	100	150	200	200	200	200	200	200	200
<u>Research-Awards</u>											
CSRS+Hatch Comp. Grants	1400	2000	3000	4000	5000	6000	7000	8000	8000	9000	9000
CSRS Fellowships	0	100	150	200	200	200	200	200	200	200	200
ARS Intramural	2250	2500	3000	4000	5000	6000	7000	8000	9000	10000	11000
SAES (State Funding)	3000	3000	4000	5000	6000	7000	8000	9000	10000	10000	10000
TOTAL COSTS	6650	8770	10850	14480	18110	21160	24160	27160	29110	32060	33010
FEDERAL COSTS	3650	5770	7850	10480	13110	15160	17160	19160	20110	22060	23010

NATIONAL ANIMAL GENOME
RESEARCH PROGRAM

APPENDIX

JUN 2 1991

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SUBJECT: National Animal Genetic Resources: CSRS/ARS Cooperative Programs

TO: John Patrick Jordan
R. D. Plowman

Recently representatives from ARS and CSRS developed the initial implementation plans for joint animal germplasm and animal genome research programs under the National Genetic Resources Program mandated by the 1990 Farm Bill. The representatives from the two agencies are applauded for their efforts. These implementation plans will serve to provide the initial groundwork for the establishment of fully integrated programs between the agencies. The critical program implementation issues were identified and dealt with in an open and forthright manner and the scientists, who will be associated with future efforts, demonstrated great enthusiasm for cooperative programs. We now have the opportunity to initiate highly visible and successful joint activities in the animal germplasm/genome areas.

Several important areas of agreement between the agencies were affirmed during these sessions. All animal germplasm and genome research activities would be included in the National Genetic Resources Program (NGRP) with a Director appointed by ARS. Interdependent and jointly coordinated programs are envisioned with ARS providing the primary leadership for animal germplasm and with CSRS giving leadership to animal genome research as shown on the enclosed organizational chart. Activities in both program areas would be closely linked and coordinated to include linkages in the advisory/technical/species committees and common databanks, as feasible. The germplasm activities would focus on beef, dairy, swine, chickens, turkeys, aquaculture species and sheep and goats, whereas, the genome activities would focus on cattle, swine, chickens, turkeys, sheep and aquaculture species. Five species coordinating centers would be designated in the Genome Program for a 10-year period. These Centers would be selected by a open deliberative process developed by CSRS and ARS Administrators utilizing an expert panel. The selection process would be open to SAES and ARS research facilities. Finally, unified future budget requests for animal germplasm/genome programs would be developed jointly by CSRS and ARS for submission to the Assistant Secretary for Science and Education.

The willingness of ARS to take a broad approach in developing the mandated Congressional report on the planning and implementation of NGRP is gratefully acknowledged. An ARS/CSRS/SAES committee has been formed to develop the animal genetic resources portion of the report. Activities will be supported by S&E Evaluation Funds through a CSRS cooperative agreement with the University of Wisconsin. This approach will allow a smooth transition from recommendations in the earlier ESCOP/ARS/CSRS report, "National Animal Genetic Resources", to the future Congressional report and to program implementation.

These implementation plans have broad implications for the future. The launching of this major scientific initiative is at a pivotal period in time. Your willingness to cooperate during this planning phase is greatly appreciated.

Charles E. Hess
Assistant Secretary
Science and Education

CHARLES E. HESS
Assistant Secretary

Enclosure

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